

IN THE CLAIMS

Please amend the claims as follows:

Claims 1-25 (Cancelled)

Claim 26 (New): An isolated polynucleotide that encodes a polypeptide which has transcription regulator LysR2 activity and which polypeptide is least 90% identical to SEQ ID NO: 2.

Claim 27 (New): The isolated polynucleotide of Claim 26, which encodes a polypeptide which is at least 95% identical to SEQ ID NO: 2.

Claim 28 (New): The isolated polynucleotide of Claim 26, which encodes a polypeptide which is at least 97% identical to SEQ ID NO: 2.

Claim 29 (New): The isolated polynucleotide of Claim 26, which encodes a polypeptide which is at least 99% identical to SEQ ID NO: 2.

Claim 30 (New): The isolated polynucleotide of Claim 26, which encodes a polypeptide which comprises SEQ ID NO: 2.

Claim 31 (New): The isolated polynucleotide of Claim 26 which is DNA.

Claim 32 (New): The isolated polynucleotide of Claim 26 which is RNA.

Claim 33 (New): An isolated polynucleotide which is at least 90% identical to SEQ ID NO: 1 and which encodes a polypeptide which has transcription regulator LysR2 activity.

Claim 34 (New): The isolated polynucleotide of Claim 33, which is at least 95% identical to SEQ ID NO: 1.

Claim 35 (New): The isolated polynucleotide of Claim 33, which is at least 99% identical to SEQ ID NO: 1.

Claim 36 (New): An isolated polynucleotide which comprises at least 15 consecutive nucleotides of SEQ ID NO: 1.

Claim 37 (New): The isolated polynucleotide of Claim 36, which comprises nucleotides 232 to 1161 of SEQ ID NO: 1.

Claim 38 (New): The isolated polynucleotide of Claim 36 which comprises SEQ ID NO: 1.

Claim 39 (New): The isolated polynucleotide of Claim 36 which encodes the polypeptide of SEQ ID NO: 2.

Claim 40 (New): An isolated polynucleotide which comprises at least 15 consecutive nucleotides of the full complement of SEQ ID NO: 1.

Claim 41 (New): A vector comprising the polynucleotide of Claim 26.

Claim 42 (New): A vector comprising the polynucleotide of Claim 30.

Claim 43 (New): A vector comprising the polynucleotide of Claim 33.

Claim 44 (New): A vector comprising the polynucleotide of Claim 36.

Claim 45 (New): A vector comprising the polynucleotide of Claim 38.

Claim 46 (New): Vector pCR2.llysR2int.

Claim 47 (New): A host cell comprising the polynucleotide of Claim 26.

Claim 48 (New): A host cell comprising the polynucleotide of Claim 30.

Claim 49 (New): A host cell comprising the polynucleotide of Claim 33.

Claim 50 (New): A host cell comprising the polynucleotide of Claim 38.

Claim 51 (New): An isolated coryneform bacterium, which expresses a decreased amount of the product of the *lysR2* gene compared to the unmodified starting strain.

Claim 52 (New): The isolated coryneform bacterium of Claim 51, wherein the *lysR2* gene has been eliminated.

Claim 53 (New): The isolated coryneform bacterium of Claim 51, wherein the *lysR2* gene has been inactivated.

Claim 54 (New): The isolated coryneform bacterium of Claim 51, wherein the *lysR2* gene has been attenuated by modification of at least one repressor gene, activator gene, operator, promoter, attenuator, ribosome binding site, start codon, start codon, or other signal structure.

Claim 55 (New): The isolated coryneform bacterium of Claim 51, wherein the *lysR2* gene has been attenuated by a modification which reduces the enzyme activity of the *lysR2* gene product.

Claim 56 (New): The isolated coryneform bacterium of Claim 51, which is of the genus *Corynebacterium* or *Brevibacterium*.

Claim 57 (New): The isolated coryneform bacterium of Claim 51, which is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium thermoaminogenes*, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and *Brevibacterium divaricatum*.

Claim 58 (New): A process for making an L-amino acid comprising:

a) culturing the bacterium of Claim 51 in an medium suitable for the production of said L-amino acid by fermentation, and

b) recovering said L-amino acid from the culture medium or from the bacterial cells.

Claim 59 (New): The process of Claim 58, wherein said amino acid is L-lysine.

Claim 60 (New): The process of Claim 58, wherein said amino acid is L-valine.

Claim 61 (New): The process of Claim 58, wherein in said bacterium the *lysR2* gene has been eliminated or inactivated.

Claim 62 (New): The process of Claim 58, wherein in said bacterium the *lysR2* gene has been attenuated by modification of at least one repressor gene, activator gene, operator, promoter, attenuator, ribosome binding site, start codon, start codon, or other signal structure.

Claim 63 (New): The process of Claim 58, wherein in said bacterium the *lysR2* gene has been attenuated by a modification which reduces the enzyme activity of the *lysR2* gene product.

Claim 64 (New): The process of Claim 58, wherein said bacterium is from the genus *Corynebacterium* or *Brevibacterium*.

Claim 65 (New): The process of Claim 58, wherein said bacterium is selected from the group consisting of *Corynebacterium glutamicum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium melassecola*, *Corynebacterium*

themoaminogenes, *Brevibacterium flavum*, *Brevibacterium lactofermentum*, and
Brevibacterium divaricatum.

Claim 66 (New): The process of Claim 58, wherein said bacterium further comprises at least one gene whose expression is enhanced (compared to an unmodified starting strain) selected from the group consisting of:

the *dapA* gene which codes for dihydrodipicolinate synthase,
the *eno* gene which codes for enolase,
the *zwf* gene which codes for the *zwf* gene product,
the *pyc* gene which codes for pyruvate carboxylase,
the *lysE* gene which codes for lysine export, and
the *lysC* gene which codes for a feed-back resistant aspartate kinase.

Claim 67 (New): The process of Claim 58, wherein said bacterium further comprises at least one gene whose expression is attenuated (compared to an unmodified starting strain) selected from the group consisting of:

the *pck* gene which codes for phosphoenol pyruvate carboxykinase,
the *pgi* gene which codes for glucose 6-phosphate isomerase,
the *poxB* gene which codes for pyruvate oxidase,
the *hom* gene which codes for homoserine dehydrogenase
the *thrB* gene which codes for homoserine kinase, and
the *panD* gene which codes for aspartate decarboxylase.